SEQUENCE LISTING

<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
Molecules and Uses Therefor

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<151> 2000-12-22

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         Arg Arg Arg Ala His Glu Arg Lys Arg Lys Leu Gln Arg Arg
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aag ctg cgc cgc agc ccg agc cgc ccg gca tcc ccg ccg cct ctg cgc   98
Lys Leu Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg
 15              20                  25                  30

ccg cgc cgc gcc ccc ggc gcc ccc tcc cca gcg cgc ccc cgg ccg ctc  146
Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
                35                  40                  45

ctc cgc gcc gcg ctc gtc ggc cat ggc ccg gga gaa cgg cga gag cag  194
Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
                50                  55                  60

ctc ctc ctg gaa aaa gca agc tga aga cat caa gaa gat ctt cga gtt  242
Leu Leu Leu Glu Lys Ala Ser  *  Arg His Gln Glu Asp Leu Arg Val
                65                  70                  75

caa aga gac cct cgg aac cgg ggc ctt ttc cga agt ggt ttt agc tga  290
Gln Arg Asp Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser  *
                80                  85                  90
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```
aga gaa ggc aac tgg caa gct ctt tgc tgt gaa gtg tat ccc taa gaa    338
Arg Glu Gly Asn Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro  *  Glu
         95              100              105

ggc gct gaa ggg caa gga aag cag cat aga gaa tga gat agc cgt cct    386
Gly Ala Glu Gly Gln Gly Lys Gln His Arg Glu  *  Asp Ser Arg Pro
         110             115              120

gag aaa gat taa gca tga aaa tat tgt tgc cct gga aga cat tta tga    434
Glu Lys Asp  *  Ala  *  Lys Tyr Cys Cys Pro Gly Arg His Leu  *
         125             130              135

aag ccc aaa tca cct gta ctt ggt cat gca gct ggt gtc cgg tgg aga    482
Lys Pro Lys Ser Pro Val Leu Gly His Ala Ala Gly Val Arg Trp Arg
             140             145              150

gct gtt tga ccg gat agt gga gaa ggg gtt tta tac aga gaa gga tgc    530
Ala Val  *  Pro Asp Ser Gly Glu Gly Val Leu Tyr Arg Glu Gly Cys
             155             160              165

cag cac tct gat ccg cca agt ctt gga cgc cgt gta cta tct cca cag    578
Gln His Ser Asp Pro Pro Ser Leu Gly Arg Arg Val Leu Ser Pro Gln
             170             175              180

aat ggg cat cgt cca cag aga cct caa gcc cga aaa tct ctt gta cta    626
Asn Gly His Arg Pro Gln Arg Pro Gln Ala Arg Lys Ser Leu Val Leu
             185             190              195

cag tca aga tga gga gtc caa aat aat gat cag tga ctt tgg att gtc    674
Gln Ser Arg  *  Gly Val Gln Asn Asn Asp Gln  *  Leu Trp Ile Val
             200             205              210

aaa aat gga ggg caa agg aga tgt gat gtc cac tgc ctg tgg aac tcc    722
Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys Leu Trp Asn Ser
             215             220              225

agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc    770
Arg Leu Cys Arg Ser  *  Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser
             230             235              240

cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg    818
Arg  *  Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg
             245             250              255

cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat    866
Leu Pro Ser Phe Leu  *   *  Lys  *  Leu Gln Ala Leu  *  Ala Asp
             260             265              270

cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc    914
Pro Gln Gly Gly Ile  *  Val  *  Leu Ser Leu Leu Gly  *  His Leu
             275             280

cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa    962
Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu
             285             290             295
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```
taa aag ata cac gtg tga gca ggc agc tcg gca ccc atg gat cgc tgg   1010
 *  Lys Ile His Val  *  Ala Gly Ser Ser Ala Pro Met Asp Arg Trp
    300                     305             310

tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat   1058
 *  His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp
    315                     320             325

ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac   1106
Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile  *  Cys His
    330                     335             340

ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga   1154
Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly
    345                     350             355

cag ttc aaa tgc aag tgt ttc gag cag cct cag ttt ggc cag cca aaa   1202
Gln Phe Lys Cys Lys Cys Phe Glu Gln Pro Gln Phe Gly Gln Pro Lys
    360                     365             370             375

aga ctg tgc gta tgt agc aaa acc aga atc cct cag ctg a cactgaagac   1252
Arg Leu Cys Val Cys Ser Lys Thr Arg Ile Pro Gln Leu
                    380             385

gagcctgggg tggagaggag ggagccggca tctgccgagc acctcctgtt tgccaggcgc  1312
tttctatact taatcccatg tcatgcgacc ctaggacttt ttttaacatg taatcactgg  1372
gccgggtgca gtggctcacg cctgtaatcc caacactttg ggaggctgag gcaggaggac  1432
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aaaatataaa aattagccgg gtgtggtggc gagcacctgt aatgtcagct acttgggagg  1552
ctgaggcagg agaatcactt gaacccagga agcggaggtt gcaatgagct gagatcacac  1612
cactgcactc cagcctgggt gacagattga gactccctct caaaaaaaaa agggaaatca  1672
ttgaacactc gtggaaccct aggtattgca tattccattt acggtttggg aatccagggc  1732
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             20              25                  30
Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu Leu Arg
         35              40                  45
Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln Leu Leu
     50              55                  60
Leu Glu Lys Ala Ser Arg His Gln Glu Asp Leu Arg Val Gln Arg Asp
65                  70                  75                  80
Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser Arg Glu Gly Asn
                 85                  90                  95
Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro Glu Gly Ala Glu Gly Gln
             100                 105                 110
Gly Lys Gln His Arg Glu Asp Ser Arg Pro Glu Lys Asp Ala Lys Tyr
             115                 120                 125
Cys Cys Pro Gly Arg His Leu Lys Pro Lys Ser Pro Val Leu Gly His
```

```
          130                        135                        140
 Ala Ala Gly Val Arg Trp Arg Ala Val Pro Asp Ser Gly Glu Gly Val
 145                      150                      155                      160
 Leu Tyr Arg Glu Gly Cys Gln His Ser Asp Pro Pro Ser Leu Gly Arg
                      165                      170                      175
 Arg Val Leu Ser Pro Gln Asn Gly His Arg Pro Gln Arg Pro Gln Ala
                  180                      185                      190
 Arg Lys Ser Leu Val Leu Gln Ser Arg Gly Val Gln Asn Asn Asp Gln
              195                      200                      205
 Leu Trp Ile Val Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys
          210                      215                      220
 Leu Trp Asn Ser Arg Leu Cys Arg Ser Ser Pro Arg Pro Glu Thr Leu
 225                      230                      235                      240
 Gln Gln Ser Arg Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala
                      245                      250                      255
 Leu Arg Leu Pro Ser Phe Leu Lys Leu Gln Ala Leu Ala Asp Pro Gln
                  260                      265                      270
 Gly Gly Ile Val Leu Ser Leu Leu Gly His Leu Arg Leu Cys Lys Arg
                  275                      280                      285
 Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu Lys Ile His Val Ala
              290                      295                      300
 Gly Ser Ser Ala Pro Met Asp Arg Trp His Ser Pro Gln Gln Lys His
 305                      310                      315                      320
 Pro Arg Val Arg Gln Arg Pro Asp Pro Glu Lys Leu Cys Gln Glu Gln
                      325                      330                      335
 Met Glu Thr Ser Ile Cys His Gly Arg Arg Glu Thr Tyr Glu Lys Thr
                  340                      345                      350
 Thr Pro Arg Gln Gln Pro Gly Gln Phe Lys Cys Lys Cys Phe Glu Gln
              355                      360                      365
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 Ile Pro Gln Leu
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gaagagaagg caactggcaa gctctttgct gtgaagtgta tccctaagaa ggcgctgaag  180
ggcaaggaaa gcagcataga gaatgagata gccgtcctga aaagattaa gcatgaaaat  240
attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggt catgcagctg  300
gtgtccggtg gagagctgtt tgaccggata gtggagaagg ggttttatac agagaaggat  360
gccagcactc tgatccgcca agtcttggac gccgtgtact atctccacag aatgggcatc  420
gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa  480
ataatgatca gtgactttgg attgtcaaaa atggagggca aggagatgt gatgtccact  540
gcctgtggaa ctccaggcta tgtcgctcct gaagtcctcg cccagaaacc ttacagcaaa  600
gccgttgact gctggtccat cggagtgatt gcctacatct tgctctgcgg ctaccctcct  660
ttttatgatg aaaatgactc caagctcttt gagcagatcc tcaaggcgga atatgagttt  720
gactctccct actgggatga catctccgac tctgcaaaag acttcattcg gaacctgatg  780
gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct  840
ggtgacacag ccctcaacaa aaacatccac gagtccgtca gcgcccagat ccggaaaaac  900
tttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga  960
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aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgtttcgag cagcctcagt 1020
ttggccagcc aaaaagactg tgcgtatgta gcaaaaccag aatccctcag ctga         1074
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tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttggag ggaaaaagta 180
cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
gctgatttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca 300
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gctgctggcg tgatcctcta tatcctgctg tgtggctttc ccccattccg cagccctgag 420
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gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
           Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
            1               5                   10
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```
gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc      1299
Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
     15                  20                  25
```

```
cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc      1347
Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
30                  35                  40                  45
```

```
aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag      1395
Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
                50                  55                  60
```

```
agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg      1443
Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
```

```
                          65                      70                      75

aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag    1491
Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
        80                      85                      90

aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc    1539
Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
        95                     100                     105

agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt    1587
Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
110                     115                     120                125

ggg gtg gag att gaa aag acc tcg ggt gaa att atc aga tgc gag aag    1635
Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys
                130                     135                     140

tgc aag aga gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt    1683
Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu
                145                     150                     155

tct ctg ggg acc agt gag ctg gat atg ggg aag ggc cca atg tat gat    1731
Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp
                160                     165                     170

gtg gag aag ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca    1779
Val Glu Lys Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala
        175                     180                     185

aat cct gca agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc    1827
Asn Pro Ala Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser
190                     195                     200                205

agc ccc agg aat ccc act caa gag ctg agg aga ccc agc aag agc atg    1875
Ser Pro Arg Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met
                210                     215                     220

gac aag aaa gag gac aga ggc cca gag gat caa gaa agc cat gct cag    1923
Asp Lys Lys Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln
                225                     230                     235

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca    1971
Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr
                240                     245                     250

gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg    2019
Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg
        255                     260                     265

agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag    2067
Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu
270                     275                     280                285

aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa    2115
Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys
                290                     295                     300
```

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aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa   2163
Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln
        305             310             315

cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag   2211
Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys
        320             325             330

cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc   2259
Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala
        335             340             345

gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg   2307
Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly
350             355             360             365

aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc   2355
Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala
                370             375             380

tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac   2403
Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp
            385             390             395

atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac   2451
Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn
        400             405             410

atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg   2499
Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu
        415             420             425

atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa   2547
Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu
430             435             440             445

agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta   2595
Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu
                450             455             460

tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac   2643
Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp
            465             470             475

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act   2691
Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr
            480             485             490

acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct   2739
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
        495             500             505

ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt   2787
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
510             515             520             525
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tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg    2835
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
            530                 535                 540

atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag    2883
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
            545                 550                 555

agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag    2931
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
            560                 565                 570

ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg    2979
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
            575                 580                 585

gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat    3027
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
590                 595                 600                 605

cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca    3075
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
                610                 615                 620

gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg    3123
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
            625                 630                 635

agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccacctt         3169
Ser Gln His Lys Arg Val Val Glu Gln Val Ser  *
            640                 645

gggaatctgt ccagccccca gttctgctca aggacagaga aaaggataga agtttgagag 3229
aaaaacaatg aaagaggctt cttcacataa ttggtgaatc agagggagag acactgagta 3289
tattttaaag catattaaaa aaattaagtc aatgttaaat gtcacaacat attttttagat 3349
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agtggtgctt accagggtct aaactccccc tgtgagatta ataaggtgca ttgtggtctt 3529
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Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser Lys Ala Leu
            35                  40                  45
Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys Ser Cys Ser
        50                  55                  60
Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly Lys Ile Pro
65                  70                  75                  80
Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly
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                     85                  90                  95
    Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala
                100                 105                 110
    Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu
                115                 120                 125
    Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg
                130                 135                 140
    Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly
    145                 150                 155                 160
    Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys
                    165                 170                 175
    Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala
                180                 185                 190
    Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg
                195                 200                 205
    Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys
                210                 215                 220
    Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala
    225                 230                 235                 240
    Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly
                    245                 250                 255
    Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His
                260                 265                 270
    Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg
                275                 280                 285
    Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys
        290                 295                 300
    Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys
    305                 310                 315                 320
    Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg
                    325                 330                 335
    Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val
                340                 345                 350
    Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala
                355                 360                 365
    Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met
        370                 375                 380
    Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp
    385                 390                 395                 400
    Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys
                    405                 410                 415
    Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu
                420                 425                 430
    Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys
        435                 440                 445
    Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala
        450                 455                 460
    Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro
    465                 470                 475                 480
    Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys
                    485                 490                 495
    Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr
                500                 505                 510
    Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys
        515                 520                 525
    Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr
        530                 535                 540
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Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln
545               550               555                   560
Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro
              565               570                   575
Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg
          580               585               590
Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu
          595               600               605
Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg
      610               615               620
Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His
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Lys Arg Val Val Glu Gln Val Ser
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<210> 6
<211> 1947
<212> DNA
<213> Human

<400> 6

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<210> 7

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence involved in ATP binding

<221> VARIANT
<222> 1
<223> The L at position 1 can be I or V.

<221> VARIANT
<222> 3
<223> The amino acid at position 3 can be any amino acid
       except P

<221> VARIANT
<222> 5
<223> The amino acid at position 3 can be any amino acid
       except P

<221> VARIANT
<222> 6
<223> The F at position 6 can be Y, W, M,G, S, T, N, or
       H

<221> VARIANT
<222> 7
<223> The S at position 7 can be G or A

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 can be any amino acid
       except P or W.

<221> VARIANT
<222> (9)...(0)
<223> The L at position 9 can be I, V, C, A, or T.

<221> VARIANT
<222> (10)...(0)
<223> The amino acid at position 10 can be any amino
       acid except P or D.

<221> VARIANT
<222> (11)...(0)
<223> The amino acid at position 11 can be any amino
       acid.

<221> VARIANT
<222> (12)...(0)

<223> The G at position 12 can be S, T, A, C, L, I, V,
      M, F, or Y.

<221> VARIANT
<222> (13)...(0)
<223> The amino acid at position 13 is as few as 5, up
      to 18, amino acids, and the amino acid can be any
      amino acid.

<221> VARIANT
<222> (14)...(0)
<223> The L at position 14 can be I, V, M, F, Y, W, C,
      S, T, A, or R.

<221> VARIANT
<222> (15)...(0)
<223> The A at position 15 can be I, V, or P.

<221> VARIANT
<222> (16)...(0)
<223> The L at position 16 can beI, V, I, M, F, A, G,
      C, K, or R.

<400> 7
Leu Gly Xaa Gly Xaa Phe Ser Xaa Leu Xaa Xaa Gly Xaa Leu Ala Leu
 1   5   10   15
Lys

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Serine/Threonine Kinase

<221> VARIANT
<222> 1
<223> The L at position 1 can be I, V, M, F, or Y.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be any amino
      acid.

<221> VARIANT
<222> 3
<223> The H at position 3 can be Y.

<221> VARIANT
<222> 4

<223> The amino acid at position 4 can be any amino
      acid.

<221> VARIANT
<222> 5
<223> The D at position 5 is an active site residue.

<221> VARIANT
<222> (6)...(0)
<223> The L at position 6 can be I, V, M, F, Y.

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 is two amino acids,
      and can be any amino acid.

<221> VARIANT
<222> (10)...(0)
<223> The L at position 10 can be any 3 of L, I, V, M,
      F, Y, C, T.

<400> 8
Leu Xaa His Xaa Asp Leu Lys Xaa Asn Leu
 1   5   10

<210> 9
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Tyrosine Kinase

<221> VARIANT
<222> 1
<223> The L at position 1 can be I, V, M, F, Y, or C.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be any amino
      acid.

<221> VARIANT
<222> 3
<223> The H at position 3 can be Y.

<221> VARIANT
<222> 4
<223> The amino acid at position 4 can be any amino
      acid.

<221> VARIANT
<222> 5
<223> The D at position 5 is an active site residue.

<221> VARIANT
<222> (6)...(0)
<223> The L at position 6 can be I, V, M, F, or Y.

<221> VARIANT
<222> (7)...(0)
<223> The R at position 7 can be S, T, A, or C.

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 is 2 amino acids, and
      can be any amino acid.

<221> VARIANT
<222> (10)...(0)
<223> The L at position 10 can be any 3 of L, I, V, M,
      F, Y, or C.

<400> 9
Leu Xaa His Xaa Asp Leu Arg Xaa Asn Leu
 1   5   10

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Tyrosine Kinase
      Phosphorylation Site

<221> VARIANT
<222> 1
<223> The R at position 1 can be K.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be two or three
      amino acids, and the amino acid can be any amino
      acid.

<221> VARIANT
<222> (3)...(0)
<223> The D at position 3 can be E.

<221> VARIANT
<222> 4
<223> The amino acid at position 2 can be two or three
      amino acids, and the amino acid can be any amino
      acid.